

Supplementary Material

Profiling bovine blastocyst microRNAs using deep sequencing

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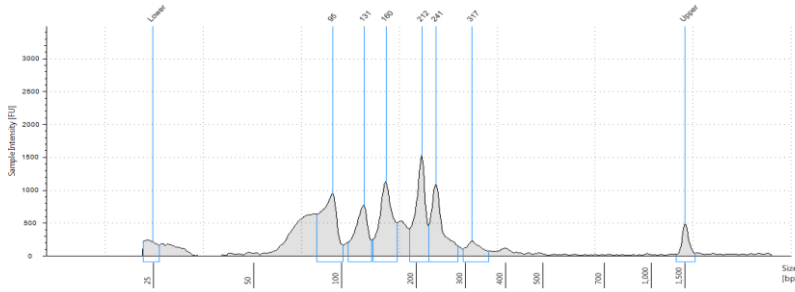
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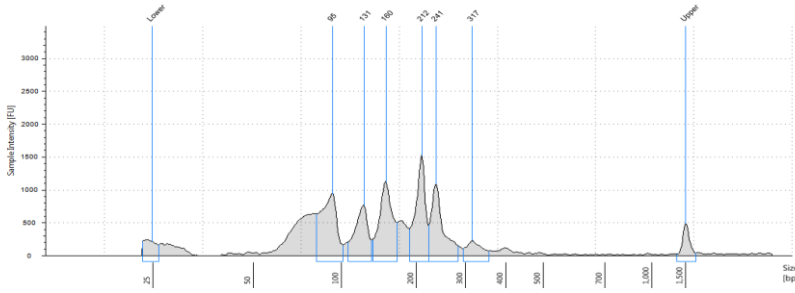
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P1A



P1B



P1C

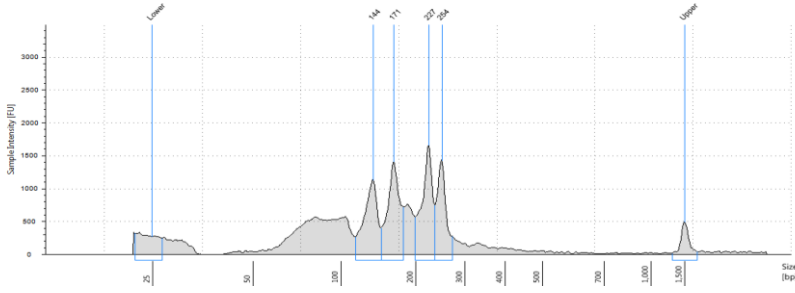
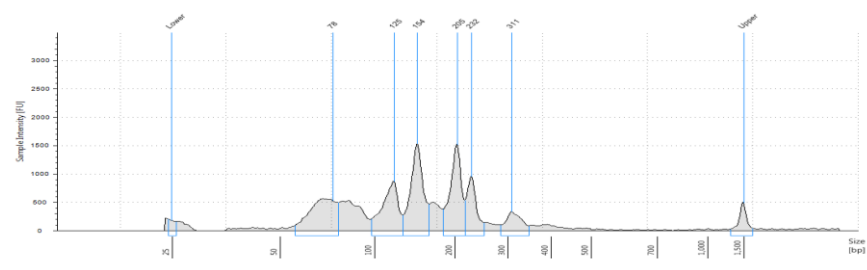


Fig. 1a

P2A



P2B

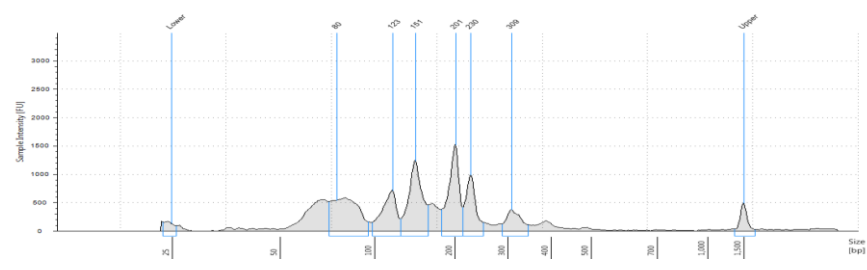


Fig. 1b

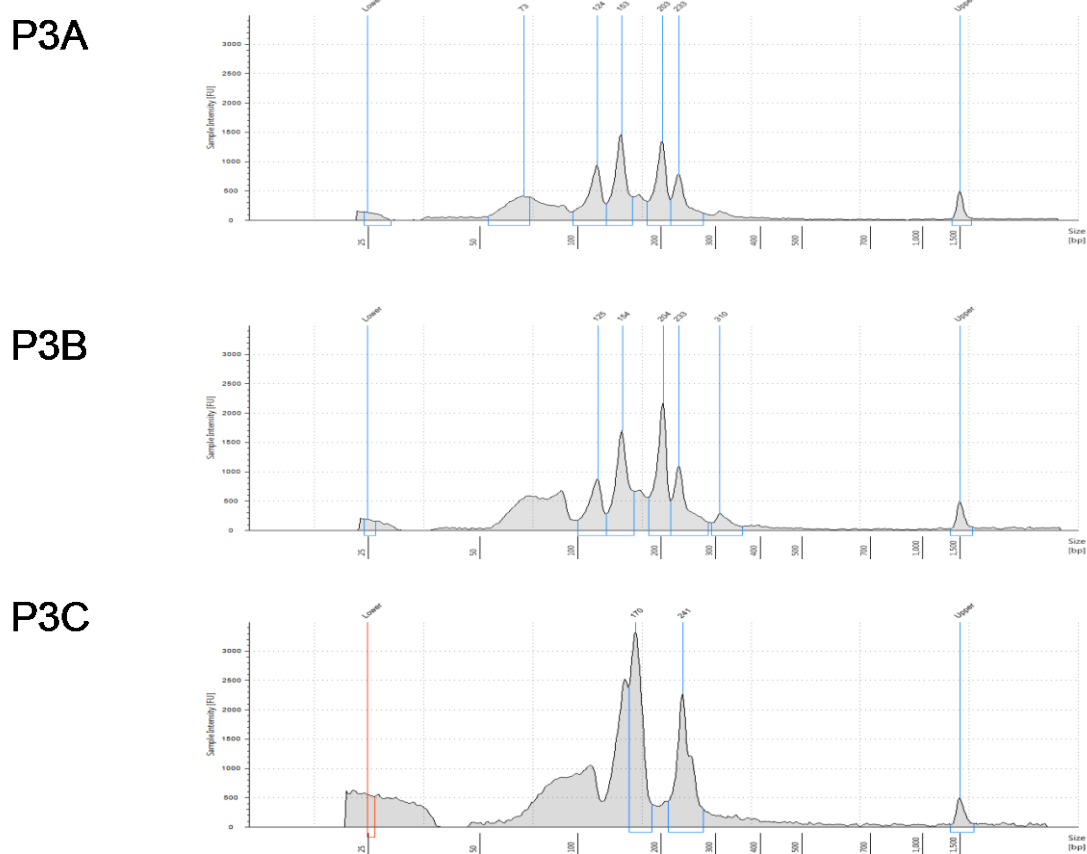


Fig. 1c

Fig. 1. Electropherograms of libraries obtained after polymerase chain reaction (PCR) amplification of 15 cycles from each sample in Procedure 1 (a), Procedure 2 (b) and Procedure 3 (c) before size selection. Lower (25 nucleotides (nt)) and upper (1500 nt) peaks indicate the ladder fragments of known length. Individual replicates (samples) are shown for each procedure.

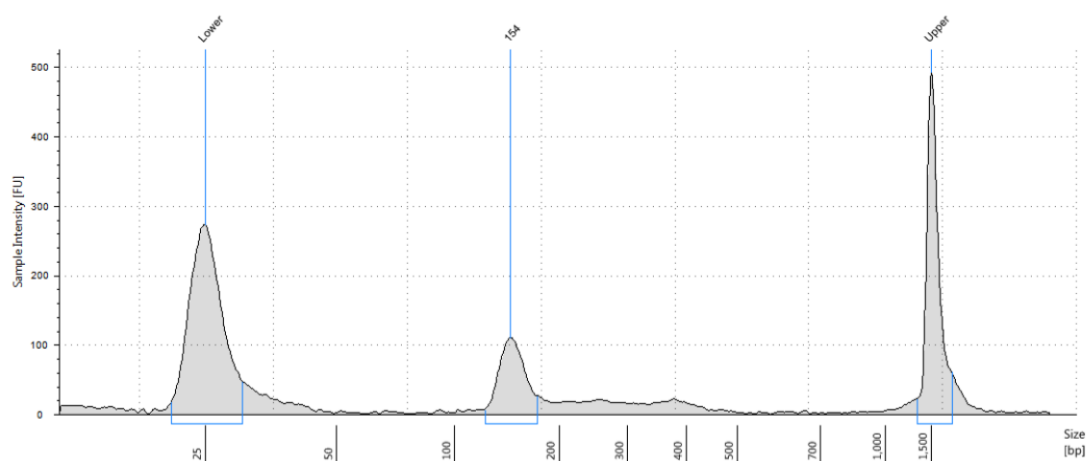


Fig. 2. Electropherograms of libraries obtained after size selection step (peak at 154 nucleotides (nt)). All eight libraries were pooled and deep sequencing was performed in a lane of an Illumina flow cell (Illumina). Lower (25 nt) and upper (1500 nt) peaks indicate the ladder fragments of known length.

Table S1. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways obtained using DIANA miRPath v2.0 are reported up to $P < 0.0001$. The target genes and homologous human miRNAs are reported for each KEGG pathways.

KEGG pathway	Target genes	miRNA ID
Cell cycle (hsa04110)	ESPL1, CDC6, GSK3B, RBL2, E2F1, SMC1A, E2F2, CDC14A, CDC25B, MCM6, CCND2, ORC1, CDKN1B, STAG2, CDKN2A, CDK6, TP53, ANAPC10, SMAD, CCNE2, E2F5, SKP2, MYC, TTK, RB1, CDC7, CDC20, BUB1B, MAD2L1, TGFB2, CCNE1, CDKN1A, CDKN2D, RAD21, MCM3, CDC25A	hsa-miR-378a-3p, hsa-miR-22-3p, hsa-miR-148a-3p, hsa-miR-92a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p
Prion diseases (hsa05020)	EGR1, PRKACA, PRNP, IL1A	hsa-miR-22-3p, hsa-miR-148a-3p, hsa-miR-191-5p, hsa-miR-423-5p, hsa-miR-192-5p
Pathways in cancer (hsa05200)	FZD7, FOS, GSK3B, STAT3, E2F1, TGFBR1, ERBB2, E2F2, BID, TCF4, APC, CRK, WNT1, RAD51, WNT5A, BCL2, CDKN1B, PLD1, WNT3, BRCA2, IGF1R, EGFR, CDKN2A, APPL1, RET, CDK6, PML, TP53, PTK2, ITGAV, FZD4, MMP2, MAPK9, SMAD4, MSH6, CCNE2, SKP2, MYC, MMP9, MSH2, PIK3R1, RB1, SOS1, HSP90B1, FGF2, FZD1, FAS, TGFB2, PPARG, NKX3-1, CCNE1, CDKN1A, CYCS, SUFU, TCF7, VEGFA, PTEN, TGFBR2, TFG	hsa-miR-378a-3p, hsa-miR-22-3p, hsa-miR-148a-3p, hsa-miR-92a-3p, hsa-miR-371a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p
Prostate cancer (hsa05215)	GSK3B, E2F1, ERBB2, E2F2, TCF4, BCL2, CDKN1B, INSR, IGF1R, EGFR, TP53, CCNE2, PIK3R1, RB1, SOS1, HSP90B1, NKX3-1, CREB3L2, CCNE1, PDGFD, CDKN1A, TCF7, PTEN	hsa-miR-22-3p, hsa-miR-148a-3p, hsa-miR-371a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p
Colorectal cancer (hsa05210)	FOS, GSK3B, TGFBR1, TCF4, APC, BCL2, APPL1, TP53, MAPK9, SMAD4, MSH6, MYC, MSH2, PIK3R1, TGFB2, CYCS, TCF7, TGFBR2	hsa-miR-378a-3p, hsa-miR-148a-3p, hsa-miR-92a-3p, hsa-miR-371a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p

Bladder cancer (hsa05219)	E2F1, ERBB2, E2F2, THBS1, EGFR, CDKN2A, RPS6KA5, TP53, MMP2, MYC, MMP9, RB1, CDKN1A, VEGFA	hsa-miR-378a-3p, hsa-miR-22-3p, hsa-miR-148a-3p, hsa-miR-92a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p
HTLV-I infection (hsa05166)	FZD7, EGR1, FOS, GSK3B, E2F1, TGFBR1, MYB, RANBP1, IL1R1, E2F2, APC, WNT1, WNT5A, CCND2, ZFP36, HLA-C, WNT3, MRAS, MAP3K1, XBP1, HLA-DOA, CDKN2A, TP53, NFATC4, RANBP3, IL15, CRTC2, FZD4, NFAT5, MAPK9, ANAPC10, SMAD4, MYC, HLA-DPA1, PRKACA, PIK3R1, RB1, ATF1, CDC20, BUB1B, MAD2L1, FZD1, HLA-G, KAT2B, TGFB2, CDKN1A, XPO1, TGFBR2	hsa-miR-378a-3p, hsa-miR-22-3p, hsa-miR-148a-3p, hsa-miR-92a-3p, hsa-miR-371a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p
Hepatitis B (hsa05161)	FOS, STAT3, E2F1, TGFBR1, E2F2, IFNB1, BCL2, CDKN1B, MAP3K1, TLR4, CDK6, DDX3X, TP53, NFATC4, APAF1, LAMTOR5, NFAT5, MAPK9, SMAD4, CNE2, MYC, MMP9, PIK3R1, RB1, FAS, TGFB2, CREB3L2, CCNE1, CDKN1A, CYCS, PTEN	hsa-miR-378a-3p, hsa-miR-22-3p, hsa-miR-148a-3p, hsa-miR-92a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p
Wnt signaling pathway (hsa04310)	FZD7, CTNNBIP1, GSK3B, TBL1X, TCF4, APC, VANGL1, WNT1, WNT5A, CCND2, ROCK2, WNT3, TP53, NFATC4, FRAT2, PRICKLE1, NLK, PLCB1, FZD4, NFAT5, MAPK9, GPC4, SMAD4, CSNK1A1, MYC, PRKACA, FZD1, PRICKLE2, TCF7, DAAM1, TBL1XR1	hsa-miR-378a-3p, hsa-miR-22-3p, hsa-miR-92a-3p, hsa-miR-371a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p
p53 signaling pathway (hsa04115)	CCNG1, ZMAT3, BID, THBS1, CCND2, PERP, CDKN2A, CDK6, TP53, APAF1, CCNE2, SESN1, MDM4, FAS, SERPINB5, CCNE1, CDKN1A, CYCS, PTEN	hsa-miR-22-3p, hsa-miR-148a-3p, hsa-miR-92a-3p, hsa-miR-26a-5p, hsa-miR-21-5p, hsa-miR-30d-5p, hsa-miR-423-5p, hsa-miR-192-5p

Table S2. Annotation cluster analysis carried out using DAVID web-tool is reported for the first 10 gene clusters identified. Each cluster is described by enrichment, which is based on an EASE score (an alternative name of Fisher Exact Statistics in DAVID system, referring to one-tailed Fisher Exact Probability Value used for gene-enrichment analysis) of each term members; the higher value represents the more enriched cluster. Moreover, GO category and term, genes associated in the cluster according to their function are reported. *P* and False Discovery Rate (FDR) were both less than 0.0001 (values not shown).

Annotation Cluster	Enrichment Score	GO Term	Genes
1	15.8	GO:0042325~regulation of phosphorylation	CCNT2, BLM, ERBB2, BMPR2, TTK, TLR4, CCNG1, PTEN, TGFB2, CCNE2, CDKN2A, CDKN2D, MAP3K1, BCL2, ILK, PRKACA, PDGFD, THBS1, FGF2, APC, EGFR, CDC6, RBL2, TGFB1, TGFB2, SMAD4, RB1, CDC25A, CDC25B, ACVR2A, ACVR2B, CDKN1A, CDKN1B, CCND2, BMP7
		GO:0051174~regulation of phosphorus metabolic process	CCNT2, BLM, ERBB2, BMPR2, TTK, TLR4, CCNG1, PTEN, TGFB2, CCNE2, CDKN2A, CDKN2D, MAP3K1, BCL2, ILK, PRKACA, PDGFD, THBS1, FGF2, APC, EGFR, CDC6, RBL2, TGFB1, TGFB2, SMAD4, RB1, CDC25A, CDC25B, ACVR2A, ACVR2B, CDKN1A, CDKN1B, CCND2, BMP7
		GO:0019220~regulation of phosphate metabolic process	CCNT2, BLM, ERBB2, BMPR2, TTK, TLR4, CCNG1, PTEN, TGFB2, CCNE2, CDKN2A, CDKN2D, MAP3K1, BCL2, ILK, PRKACA, PDGFD, THBS1, FGF2, APC, EGFR, CDC6, RBL2, TGFB1, TGFB2, SMAD4, RB1, CDC25A, CDC25B, ACVR2A, ACVR2B, CDKN1A, CDKN1B, CCND2, BMP7
2	14.3	GO:0043067~regulation of programmed cell death	BID, MMP9, ZMAT3, ERBB2, BTC, PML, TLR4, PTEN, TGFB2, IGF1R, CDKN2A, CDKN2D, SOS1, MAP3K1, BCL2, ILK, FAS, THBS1, MYC, FGF2, IL1A, APC, EGFR, MSH6, MSH2, TGFB1, CYCS, SKP2, TP53, BRCA2, BRCA1, HSP90B1, CDKN1A, CDKN1B, IFNB1, GSK3B, VEGFA, MAPK9, APAF1, NGFR, PRNP, PERP, BMP7
		GO:0010941~regulation of cell death	BID, MMP9, ZMAT3, ERBB2, BTC, PML, TLR4, PTEN, TGFB2, IGF1R, CDKN2A, CDKN2D, SOS1, MAP3K1, BCL2, ILK, FAS, THBS1, MYC, FGF2, IL1A, APC, EGFR, MSH6, MSH2, TGFB1, CYCS, SKP2, TP53, BRCA2, BRCA1, HSP90B1, CDKN1A, CDKN1B, IFNB1, GSK3B, VEGFA, MAPK9, APAF1, NGFR, PRNP, PERP, BMP7
		GO:0042981~regulation of apoptosis	BID, MMP9, ZMAT3, ERBB2, BTC, PML, TLR4, PTEN, TGFB2, IGF1R, CDKN2A, CDKN2D, SOS1, MAP3K1, BCL2, ILK, FAS, THBS1, MYC, IL1A, APC, EGFR, MSH6, MSH2, TGFB1, CYCS, SKP2, TP53, BRCA2, BRCA1, HSP90B1, CDKN1A, CDKN1B, IFNB1, GSK3B, VEGFA, MAPK9, APAF1, NGFR, PRNP, PERP, BMP7

3	14.1	GO:0005654~nucleoplasm	CCNT2, E2F1, E2F2, SUPT3H, XPO1, BLM, E2F5, PML, ANAPC10, ATF1, CCNE2, CCNE1, FOS, CDKN2A, DDX3X, FANCI, HOXA9, TCF4, POLQ, RUNX2, MYC, ERCC4, CDC7, TBL1XR1, CDC6, KAT2B, RBL2, USP1, TP53, SMAD4, BRCA2, CDC20, RB1, SMAD1, APPL1, MCP3, BRCA1, CDC25A, CDC25B, RAD51, MCM6, RPS6KA5, CDKN1A, PBX1, NGFR, TBL1X
		GO:0031981~nuclear lumen	E2F1, CCNT2, E2F2, XPO1, E2F5, ZMAT3, CCNE2, FOS, CCNE1, CDKN2A, FANCI, MYB, MYC, CDC7, CDC6, TBL1XR1, RBL2, USP1, TP53, RB1, MCP3, RAD51, MCM6, NGFR, SUPT3H, BLM, PML, ANAPC10, SUFU, ATF1, DDX3X, HOXA9, POLQ, TCF4, RUNX2, ERCC4, KAT2B, NLK, EME1, SMAD4, BRCA2, CDC20, SMAD1, APPL1, BRCA1, CDC25A, STAT3, CDC25B, RPS6KA5, CDKN1A, SP1, PBX1, TBL1X
		GO:0043233~organelle lumen	E2F1, CCNT2, E2F2, XPO1, E2F5, ZMAT3, TGFB2, CCNE2, FOS, CCNE1, CDKN2A, FANCI, MYB, MYC, CDC7, CDC6, TBL1XR1, RBL2, USP1, CYCS, TP53, RB1, MCP3, RAD51, MCM6, VEGFA, NGFR, SUPT3H, BLM, PML, ANAPC10, SUFU, ATF1, DDX3X, HOXA9, POLQ, TCF4, THBS1, RUNX2, ERCC4, KAT2B, NLK, EME1, SMAD4, BRCA2, CDC20, SMAD1, APPL1, STAT3, CDC25A, BRCA1, CDC25B, RPS6KA5, HSP90B1, CDKN1A, SP1, PBX1, TBL1X
		GO:0031974~membrane-enclosed lumen	E2F1, CCNT2, E2F2, XPO1, E2F5, ZMAT3, TGFB2, CCNE2, FOS, CCNE1, CDKN2A, FANCI, MYB, MYC, CDC7, CDC6, TBL1XR1, RBL2, USP1, CYCS, TP53, RB1, MCP3, RAD51, MCM6, VEGFA, NGFR, SUPT3H, BLM, PML, ANAPC10, SUFU, ATF1, DDX3X, HOXA9, POLQ, TCF4, THBS1, RUNX2, ERCC4, KAT2B, NLK, EME1, SMAD4, BRCA2, CDC20, SMAD1, APPL1, STAT3, CDC25A, BRCA1, CDC25B, RPS6KA5, HSP90B1, CDKN1A, SP1, PBX1, TBL1X
		GO:0070013~intracellular organelle lumen	E2F1, CCNT2, E2F2, XPO1, E2F5, ZMAT3, CCNE2, FOS, CCNE1, CDKN2A, FANCI, MYB, MYC, CDC7, CDC6, TBL1XR1, RBL2, USP1, CYCS, TP53, RB1, MCP3, RAD51, MCM6, NGFR, SUPT3H, BLM, PML, ANAPC10, SUFU, ATF1, DDX3X, HOXA9, POLQ, TCF4, RUNX2, ERCC4, KAT2B, NLK, EME1, SMAD4, BRCA2, CDC20, SMAD1, APPL1, STAT3, BRCA1, CDC25A, CDC25B, RPS6KA5, HSP90B1, CDKN1A, SP1, PBX1, TBL1X
4	12.4	GO:0002520~immune system development	BLM, MMP9, PPARG, PML, IL15, TGFB2, BCL2, HOXA9, FAS, PIK3R1, APC, EGR1, MSH6, MSH2, TGFB1, TGFB2, TP53, BRCA2, CDK6, RB1, SIX4, ID2, SP1, VEGFA, PBX1
		GO:0048534~hemopoietic or lymphoid organ development	EGR1, BLM, MSH2, MMP9, TGFB1, PPARG, TGFB2, TP53, PML, BRCA2, CDK6, RB1, IL15, SIX4, TGFB2, SP1, ID2, BCL2, VEGFA, HOXA9, PBX1, FAS, PIK3R1, APC
		GO:0030097~hemopoiesis	EGR1, BLM, MSH2, MMP9, PPARG, TGFB2, TP53, PML, BRCA2, CDK6, RB1, IL15, TGFB2, ID2, SP1, BCL2, VEGFA, HOXA9, PBX1, FAS, PIK3R1, APC
5	12.2	GO:0051338~regulation of transferase activity	CCNT2, BLM, ERBB2, PPARG, CCNG1, PTEN, TGFB2, CCNE2, CDKN2A, MAP3K1, CDKN2D, ILK, PRKACA, THBS1, FGF2, APC, EGFR, CDC6, RBL2, TGFB1, TGFB2, RB1, CDC25A, CDC25B, ACVR2B, CDKN1A, CDKN1B, CCND2

		GO:0043549~regulation of kinase activity	CCNT2, BLM, ERBB2, CCNG1, PTEN, TGFB2, CCNE2, CDKN2A, MAP3K1, CDKN2D, ILK, PRKACA, THBS1, FGF2, APC, EGFR, CDC6, RBL2, TGFB1, TGFB2, RB1, CDC25A, CDC25B, ACVR2B, CDKN1A, CDKN1B, CCND2
		GO:0045859~regulation of protein kinase activity	CCNT2, BLM, ERBB2, CCNG1, PTEN, TGFB2, CCNE2, CDKN2A, MAP3K1, CDKN2D, ILK, PRKACA, THBS1, FGF2, APC, EGFR, CDC6, TGFB1, TGFB2, RB1, CDC25A, CDC25B, ACVR2B, CDKN1A, CDKN1B, CCND2
6	11.2	kinase	ERBB2, BMPR2, TFG, TTK, RPS6KB1, INSR, PAK6, IGF1R, PTK2, CDKN2A, MAP3K1, ILK, PRKACA, CDK14, CDC7, EGFR, CSNK1A1, RET, ROCK2, NLK, TGFB1, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, CDKN1A, CDKN1B, GSK3B, BMP2K, BUB1B, MAPK9, PLAU
		binding site:ATP	ERBB2, BMPR2, TTK, RPS6KB1, INSR, PAK6, IGF1R, PTK2, MAP3K1, ILK, PRKACA, CDK14, EGFR, CSNK1A1, CDC7, RET, ROCK2, TGFB1, NLK, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, HSP90B1, GSK3B, BMP2K, BUB1B, MAPK9
		domain:Protein kinase	ERBB2, BMPR2, TTK, RPS6KB1, INSR, PAK6, IGF1R, PTK2, MAP3K1, ILK, PRKACA, CDK14, EGFR, CSNK1A1, CDC7, RET, ROCK2, TGFB1, NLK, TGFB2, CDK6, ACVR2A, ACVR2B, GSK3B, BMP2K, BUB1B, MAPK9
		IPR017441:Protein kinase, ATP binding site	ERBB2, BMPR2, TFG, TTK, RPS6KB1, INSR, PAK6, IGF1R, PTK2, MAP3K1, ILK, PRKACA, CDK14, EGFR, CSNK1A1, CDC7, RET, ROCK2, TGFB1, NLK, CDK6, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, BUB1B, MAPK9
		IPR000719:Protein kinase, core	ERBB2, BMPR2, TFG, TTK, RPS6KB1, INSR, PAK6, IGF1R, PTK2, MAP3K1, ILK, PRKACA, CDK14, EGFR, CSNK1A1, CDC7, RET, ROCK2, TGFB1, NLK, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, MAPK9
		GO:0004672~protein kinase activity	ERBB2, BMPR2, TFG, TTK, RPS6KB1, TGFB2, INSR, PAK6, IGF1R, PTK2, MAP3K1, ILK, PRKACA, CDK14, CDC7, EGFR, CSNK1A1, RET, ROCK2, TGFB1, NLK, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, BUB1B, MAPK9
		active site:Proton acceptor	ERBB2, BMPR2, TTK, RPS6KB1, INSR, PAK6, IGF1R, PTK2, MAP3K1, PRKACA, CDK14, EGFR, CSNK1A1, CDC7, RET, ROCK2, TGFB1, NLK, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, BUB1B, MAPK9
		transferase	ERBB2, BMPR2, TFG, TTK, RPS6KB1, INSR, PAK6, IGF1R, PTK2, MAP3K1, ILK, PRKACA, CDK14, CDC7, EGFR, CSNK1A1, RET, KAT2B, REV1, ROCK2, NLK, TGFB1, TGFB2, CDK6, WHSC1, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, BUB1B, MAPK9, REV3L
7	10.5	IPR000719:Protein kinase, core	ERBB2, BMPR2, TFG, TTK, RPS6KB1, INSR, PAK6, IGF1R, PTK2, MAP3K1, ILK, PRKACA, CDK14, EGFR, CSNK1A1, CDC7, RET, ROCK2, TGFB1, NLK, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, MAPK9

		GO:0006468~protein amino acid phosphorylation	ERBB2, BMPR2, PML, TFG, TTK, RPS6KB1, INSR, TGFB2, PAK6, IGF1R, PTK2, MAP3K1, BCL2, ILK, PRKACA, THBS1, FGF2, CDK14, CDC7, CSNK1A1, EGFR, RET, ROCK2, NLK, TGFB1, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, MAPK9, BMP7
		GO:0006796~phosphate metabolic process	CDC14A, ERBB2, PML, BMPR2, TTK, TFG, RPS6KB1, PTEN, INSR, TGFB2, PAK6, IGF1R, PTK2, MAP3K1, BCL2, ILK, PRKACA, THBS1, FGF2, CDK14, PIK3R1, CDC7, CSNK1A1, EGFR, RET, ROCK2, MSH2, NLK, TGFB1, TGFB2, CDK6, CDC25A, CDC25B, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, MAPK9, BMP7
		GO:0006793~phosphorus metabolic process	CDC14A, ERBB2, PML, BMPR2, TTK, TFG, RPS6KB1, PTEN, INSR, TGFB2, PAK6, IGF1R, PTK2, MAP3K1, BCL2, ILK, PRKACA, THBS1, FGF2, CDK14, PIK3R1, CDC7, CSNK1A1, EGFR, RET, ROCK2, MSH2, NLK, TGFB1, TGFB2, CDK6, CDC25A, CDC25B, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, MAPK9, BMP7
		GO:0016310~phosphorylation	ERBB2, BMPR2, PML, TTK, TFG, RPS6KB1, INSR, TGFB2, PAK6, IGF1R, PTK2, MAP3K1, BCL2, ILK, PRKACA, THBS1, FGF2, CDK14, PIK3R1, CDC7, CSNK1A1, EGFR, RET, MSH2, ROCK2, NLK, TGFB1, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, MAPK9, BMP7
		GO:0004672~protein kinase activity	ERBB2, BMPR2, TFG, TTK, RPS6KB1, TGFB2, INSR, PAK6, IGF1R, PTK2, MAP3K1, ILK, PRKACA, CDK14, CDC7, EGFR, CSNK1A1, RET, ROCK2, TGFB1, NLK, TGFB2, CDK6, RPS6KA5, ACVR2A, ACVR2B, GSK3B, BMP2K, BUB1B, MAPK9
8	10.4	GO:0043065~positive regulation of apoptosis	BID, MMP9, ZMAT3, PML, TLR4, PTEN, TGFB2, CDKN2A, MAP3K1, BCL2, SOS1, FAS, MYC, APC, MSH6, TGFB1, TP53, SKP2, BRCA2, BRCA1, CDKN1A, CDKN1B, IFNB1, MAPK9, NGFR, BMP7, PERP
		GO:0043068~positive regulation of programmed cell death	BID, MMP9, ZMAT3, PML, TLR4, PTEN, TGFB2, CDKN2A, MAP3K1, BCL2, SOS1, FAS, MYC, APC, MSH6, TGFB1, TP53, SKP2, BRCA2, BRCA1, CDKN1A, CDKN1B, IFNB1, MAPK9, NGFR, BMP7, PERP
		GO:0010942~positive regulation of cell death	BID, MMP9, ZMAT3, PML, TLR4, PTEN, TGFB2, CDKN2A, MAP3K1, BCL2, SOS1, FAS, MYC, APC, MSH6, TGFB1, TP53, SKP2, BRCA2, BRCA1, CDKN1A, CDKN1B, IFNB1, MAPK9, NGFR, BMP7, PERP
9	9.4	GO:0051272~positive regulation of cell motion	EGFR, PLD1, MMP9, TGFB1, RPS6KB1, TGFB2, IGF1R, BCL2, ILK, VEGFA, HBEGF, THBS1, FGF2, PIK3R1, APC
		GO:0030335~positive regulation of cell migration	EGFR, PLD1, MMP9, RPS6KB1, TGFB2, IGF1R, BCL2, VEGFA, ILK, HBEGF, THBS1, FGF2, PIK3R1, APC
		GO:0040017~positive regulation of locomotion	EGFR, PLD1, MMP9, RPS6KB1, TGFB2, IGF1R, BCL2, VEGFA, ILK, HBEGF, THBS1, FGF2, PIK3R1, APC

10		GO:0051270~regulation of cell motion	EGFR, PLD1, MMP9, TGFB1, RPS6KB1, PTEN, TGFB2, IGF1R, CDKN1B, BCL2, MAP3K1, ILK, VEGFA, HBEGF, THBS1, FGF2, PIK3R1, APC
		GO:0040012~regulation of locomotion	EGFR, PLD1, MMP9, RPS6KB1, PTEN, TGFB2, IGF1R, IFNB1, BCL2, MAP3K1, ILK, VEGFA, HBEGF, THBS1, FGF2, PIK3R1, APC
		GO:0030334~regulation of cell migration	EGFR, PLD1, MMP9, RPS6KB1, PTEN, TGFB2, IGF1R, BCL2, MAP3K1, ILK, VEGFA, HBEGF, THBS1, FGF2, PIK3R1, APC
	9.1	GO:0010557~positive regulation of macromolecule biosynthetic process	E2F1, BLM, PPARG, TLR4, TGFB2, CCNE1, FOS, WNT1, IGF1R, MAP3K1, NFAT5, TCF4, THBS1, FGF2, MYC, RUNX2, IL1A, EGR1, TBL1XR1, TGFB1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, BRCA1, STAT3, SP1, VEGFA, PBX1, BMP7, TBL1X
		GO:0009891~positive regulation of biosynthetic process	E2F1, BLM, PPARG, TLR4, TGFB2, CCNE1, FOS, WNT1, IGF1R, MAP3K1, NFAT5, TCF4, THBS1, FGF2, MYC, RUNX2, IL1A, EGR1, EGFR, TBL1XR1, TGFB1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, BRCA1, STAT3, SP1, VEGFA, PBX1, BMP7, TBL1X
		GO:0031328~positive regulation of cellular biosynthetic process	E2F1, BLM, PPARG, TLR4, CCNE1, FOS, WNT1, IGF1R, MAP3K1, NFAT5, TCF4, THBS1, FGF2, MYC, RUNX2, IL1A, EGFR, EGR1, TBL1XR1, TGFB1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, BRCA1, STAT3, SP1, VEGFA, PBX1, BMP7, TBL1X
		GO:0051173~positive regulation of nitrogen compound metabolic process	E2F1, BLM, PPARG, CCNE1, FOS, WNT1, IGF1R, MAP3K1, NFAT5, TCF4, FGF2, MYC, RUNX2, EGFR, EGR1, TBL1XR1, TGFB1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, BRCA1, STAT3, RAD51, SP1, VEGFA, PBX1, BMP7, TBL1X
		GO:0010628~positive regulation of gene expression	E2F1, BLM, PPARG, CCNE1, FOS, WNT1, MAP3K1, NFAT5, TCF4, FGF2, MYC, RUNX2, EGR1, TBL1XR1, TGFB1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, STAT3, BRCA1, SP1, VEGFA, MAPK9, PBX1, BMP7, TBL1X
		GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	E2F1, BLM, PPARG, CCNE1, FOS, WNT1, IGF1R, MAP3K1, NFAT5, TCF4, FGF2, MYC, RUNX2, EGR1, TBL1XR1, TGFB1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, BRCA1, STAT3, RAD51, SP1, VEGFA, PBX1, BMP7, TBL1X
		GO:0045893~positive regulation of transcription, DNA-dependent	E2F1, PPARG, FOS, WNT1, CCNE1, MAP3K1, NFAT5, TCF4, FGF2, MYC, RUNX2, EGR1, TBL1XR1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, STAT3, BRCA1, SP1, VEGFA, PBX1, BMP7, TBL1X

		GO:0051254~positive regulation of RNA metabolic process	E2F1, PPARG, FOS, WNT1, CCNE1, MAP3K1, NFAT5, TCF4, FGF2, MYC, RUNX2, EGR1, TBL1XR1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, STAT3, BRCA1, SP1, VEGFA, PBX1, BMP7, TBL1X
		GO:0045941~positive regulation of transcription	E2F1, BLM, PPARG, FOS, WNT1, CCNE1, MAP3K1, NFAT5, TCF4, FGF2, MYC, RUNX2, EGR1, TBL1XR1, TGFBR1, SMAD4, TP53, RB1, SMAD1, NR4A3, SIX4, STAT3, BRCA1, SP1, VEGFA, PBX1, BMP7, TBL1X
		GO:0045944~positive regulation of transcription from RNA polymerase II promoter	E2F1, EGR1, TBL1XR1, PPARG, TP53, SMAD4, RB1, NR4A3, SMAD1, SIX4, STAT3, FOS, SP1, MAP3K1, VEGFA, NFAT5, PBX1, BMP7, TBL1X, FGF2, RUNX2, MYC